What is claimed is:

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1. An antagonist that inhibits or an agonist that activates an activity a polypeptide selected from the group consisting of: a polypeptide comprising an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO:2 or 4, and a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or 4, wherein said activity is selected from the group consisting of:

uncompetitive inhibition by Apo-ACP versus NADH (Ki(app); competitive inhibition by Apo-ACP versus crotonoyl CoA; induction of negative cooperativity with respect to CCA binding;

use of NADH and NADPH as substrates by Fab I;
binding of NADH and NADPH by FabI;
oxidation of NADH and NADPH by FabI;
ratio of Kmapp for NADH as compared to NADPH;

use of NADH and crotonoyl CoA as substrates by Fab I in a sequential

kinetic mechanism;
sequential binding of NADH and crotonoyl CoA by Fab I;
increasing inhibition of FabI by saturated fatty acyl CoA's of increasing chain length;

feedback regulatory mechanism of Fab I by saturated fatty acyl CoA's;

competitive inhibition by palmitoyl CoA versus crotonoyl CoA; competitive inhibition by palmitoyl CoA versus crotonoyl CoA modulation through binding of multiple palmitoyl CoA molecules to Fab I; binding of multiple palmitoyl CoA molecules to Fab I;

negative cooperativity in the binding of CCA:

formation of an dimeric quaternary structure;
formation of an tetrameric quaternary structure;
formation of an oligomeric quaternary structure;
binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitoyl

coA; and

NADH binding to Fab I prior to or simultaneous with ACP binding.

2. A method for the treatment of an individual having need to inhibit or activate Fab I polypeptide comprising the steps of: administering to the individual a antibacterially

effective amount of an antagonist that inhibits or an agonist that activates an activity of a polypeptide selected from the group consisting of: a polypeptide comprising an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO:2 or 4, and a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or 4, wherein said activity is selected from the group consisting of:

uncompetitive inhibition by Apo-ACP versus NADH (Ki(app); competitive inhibition by Apo-ACP versus crotonoyl CoA; induction of negative cooperativity with respect to CCA binding; use of NADH and NADPH as substrates by Fab I;

binding of NADH and NADPH by FabI;
oxidation of NADH and NADPH by FabI;
ratio of Kmapp for NADH as compared to NADPH;
use of NADH and crotonoyl CoA as substrates by Fab I in a sequential kinetic mechanism;

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sequential binding of NADH and crotonoyl CoA by Fab I; increasing inhibition of FabI by saturated fatty acyl CoA's of increasing chain length;

feedback regulatory mechanism of Fab I by saturated fatty acyl CoA's; competitive inhibition by palmitoyl CoA versus crotonoyl CoA;

competitive inhibition by palmitoyl CoA versus crotonoyl CoA modulation through binding of multiple palmitoyl CoA molecules to Fab I; binding of multiple palmitoyl CoA molecules to Fab I; negative cooperativity in the binding of CCA; formation of an dimeric quaternary structure:

formation of an tetrameric quaternary structure:

formation of an oligomeric quaternary structure;

binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitoyl coA; and

NADH binding to Fab I prior to or simultaneous with ACP binding.

30 3. A method for the treatment of an individual infected with a bacteria comprising the steps of administering to the individual a antibacterially effective amount of an antagonist that inhibits or an agonist that activates an activity of a polypeptide selected from

the group consisting of: a polypeptide comprising an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO:2 or 4, and a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or 4, wherein said activity is selected from the group consisting of:

- uncompetitive inhibition by Apo-ACP versus NADH (Ki(app); competitive inhibition by Apo-ACP versus crotonoyl CoA; induction of negative cooperativity with respect to CCA binding; use of NADH and NADPH as substrates by Fab I; binding of NADH and NADPH by FabI;
- oxidation of NADH and NADPH by FabI:
 ratio of Kmapp for NADH as compared to NADPH:
 use of NADH and crotonoyl CoA as substrates by Fab I in a sequential kinetic mechanism;
 sequential binding of NADH and crotonoyl CoA by Fab I;
- increasing inhibition of FabI by saturated fatty acyl CoA's of increasing chain length; feedback regulatory mechanism of Fab I by saturated fatty acyl CoA's;

competitive inhibition by palmitoyl CoA versus crotonoyl CoA; competitive inhibition by palmitoyl CoA versus crotonoyl CoA modulation

- through binding of multiple palmitoyl CoA molecules to Fab I; binding of multiple palmitoyl CoA molecules to Fab I; negative cooperativity in the binding of CCA; formation of an dimeric quaternary structure; formation of an tetrameric quaternary structure;
- formation of an oligomeric quaternary structure;
 binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitoyl coA; and

NADH binding to Fab I prior to or simultaneous with ACP binding.

4. The method of claim 3 wherein said bacteria is selected from the group consisting of a member of the genus *Staphylococcus*, *Staphylococcus* aureus, a member of the genus *Streptococcus*, and *Streptococcus* pneumoniae.

5. A method for the treatment of an individual having need to inhibit or activate Fab I polypeptide comprising the steps of administering to the individual a antibacterially effective amount of an antagonist that inhibits or an agoinist that activates an activity of Fab I selected from the group consisting of:

- uncompetitive inhibition by Apo-ACP versus NADH (Ki(app); competitive inhibition by Apo-ACP versus crotonoyl CoA; induction of negative cooperativity with respect to CCA binding; use of NADH and NADPH as substrates by Fab I; binding of NADH and NADPH by FabI;
- oxidation of NADH and NADPH by FabI;
 ratio of Kmapp for NADH as compared to NADPH;
 use of NADH and crotonoyl CoA as substrates by Fab I in a sequential kinetic mechanism;

sequential binding of NADH and crotonoyl CoA by Fab I;

increasing inhibition of FabI by saturated fatty acyl CoA's of increasing chain length; feedback regulatory mechanism of FabI by saturated fatty acyl CoA's;

competitive inhibition by palmitoyl CoA versus crotonoyl CoA; competitive inhibition by palmitoyl CoA versus crotonoyl CoA modulation

through binding of multiple palmitoyl CoA molecules to Fab I; binding of multiple palmitoyl CoA molecules to Fab I; negative cooperativity in the binding of CCA; formation of an dimeric quaternary structure;

formation of an tetrameric quaternary structure;

formation of an oligomeric quaternary structure;
binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitoyl
coA; and

NADH binding to Fab I prior to or simultaneous with ACP binding.

6. A method for the treatment of an individual infected with a bacteria comprising the steps of administering to the individual a antibacterially effective amount of an antagonist that inhibits or an agonist that activates that activates an activity of Fab I selected from the group consisting of:

uncompetitive inhibition by Apo-ACP versus NADH (Ki(app); competitive inhibition by Apo-ACP versus crotonoyl CoA: induction of negative cooperativity with respect to CCA binding; use of NADH and NADPH as substrates by Fab I: 5 binding of NADH and NADPH by Fabl; oxidation of NADH and NADPH by Fabl; ratio of Kmapp for NADH as compared to NADPH; use of NADH and crotonovl CoA as substrates by Fab I in a sequential kinetic mechanism: 10 sequential binding of NADH and crotonovl CoA by Fab I; increasing inhibition of Fabl by saturated fatty acyl CoA's of increasing chain length; feedback regulatory mechanism of Fab I by saturated fatty acyl CoA's; competitive inhibition by palmitoyl CoA versus crotonoyl CoA; 15 competitive inhibition by palmitoyl CoA versus crotonoyl CoA modulation through binding of multiple palmitoyl CoA molecules to Fab I: binding of multiple palmitoyl CoA molecules to Fab I; negative cooperativity in the binding of CCA; formation of an dimeric quaternary structure; 20 formation of an tetrameric quaternary structure; formation of an oligomeric quaternary structure; binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitovl coA; and

NADH binding to Fab I prior to or simultaneous with ACP binding.

- 7. The method of claim 6 wherein said bacteria is selected from the group consisting of: a member of the genus *Staphylococcus*, *Staphylococcus aureus*, a member of the genus *Streptococcus*, and *Streptococcus pneumoniae*.
 - 8. A method for the treatment of an individual infected by *Streptococcus pneumoniae* comprising the steps of administering to the individual a antibacterially effective amount of an antagonist that inhibits or anagonist that activates an activity of *Streptococcus pneumoniae* Fab I selected from the group consisting of:

uncompetitive inhibition by Apo-ACP versus NADH (Ki(app);

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competitive inhibition by Apo-ACP versus crotonovl CoA: induction of negative cooperativity with respect to CCA binding: use of NADH and NADPH as substrates by Fab I; binding of NADH and NADPH by Fabl: 5 oxidation of NADH and NADPH by Fabl; ratio of Kmapp for NADH as compared to NADPH; use of NADH and crotonovl CoA as substrates by Fab I in a sequential kinetic mechanism: sequential binding of NADH and crotonovl CoA by Fab I; 10 increasing inhibition of Fabl by saturated fatty acvl CoA's of increasing chain length; feedback regulatory mechanism of Fab I by saturated fatty acvl CoA's; competitive inhibition by palmitoyl CoA versus crotonoyl CoA: competitive inhibition by palmitoyl CoA versus crotonoyl CoA modulation through binding of multiple palmitoyl CoA molecules to Fab I; 15 binding of multiple palmitoyl CoA molecules to Fab I: negative cooperativity in the binding of CCA: formation of an dimeric quaternary structure; formation of an tetrameric quaternary structure; 20 formation of an oligomeric quaternary structure: binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitoyl coA; and NADH binding to Fab I prior to or simultaneous with ACP binding. 9. An antagonist that inhibits an activity of a polypeptide selected from the 25 group consisting of: a polypeptide comprising an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO:2 or 4, and a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or 4, , wherein said activity is selected from

uncompetitive inhibition by Apo-ACP versus NADH (Ki(app);

competitive inhibition by Apo-ACP versus crotonoyl CoA; induction of negative cooperativity with respect to CCA binding; use of NADH and NADPH as substrates by Fab I;

the group consisting of:

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binding of NADH and NADPH by Fabl; oxidation of NADH and NADPH by FabI: ratio of Kmapp for NADH as compared to NADPH; use of NADH and crotonovl CoA as substrates by Fab I in a sequential 5 kinetic mechanism: sequential binding of NADH and crotonovl CoA by Fab I; increasing inhibition of Fabl by saturated fatty acyl CoA's of increasing chain length; feedback regulatory mechanism of Fab I by saturated fatty acyl CoA's; 10 competitive inhibition by palmitovl CoA versus crotonovl CoA; competitive inhibition by palmitovl CoA versus crotonovl CoA modulation through binding of multiple palmitovl CoA molecules to Fab I; binding of multiple palmitoyl CoA molecules to Fab I; negative cooperativity in the binding of CCA; 15 formation of an dimeric quaternary structure; formation of an tetrameric quaternary structure; formation of an oligomeric quaternary structure; binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitoyl coA; and 20 NADH binding to Fab I prior to or simultaneous with ACP binding. 10. A method for the treatment of an individual having need to inhibit Fab I polypeptide comprising the steps of administering to the individual a antibacterially effective amount of an antagonist that inhibits an activity of a polypeptide selected from the group consisting of a polypeptide comprising an amino acid sequence which is at least 90% 25 identical to the amino acid sequence of SEQ ID NO:2 or 4, and a polypeptide comprising an amino acid sequence as set forth in SEQ ID NO:2 or 4, , wherein said activity is selected from the group consisting of: uncompetitive inhibition by Apo-ACP versus NADH (Ki(app);

competitive inhibition by Apo-ACP versus crotonoyl CoA; induction of negative cooperativity with respect to CCA binding; use of NADH and NADPH as substrates by Fab I;

binding of NADH and NADPH by FabI;

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oxidation of NADH and NADPH by Fabl; ratio of Kmapp for NADH as compared to NADPH; use of NADH and crotonovl CoA as substrates by Fab I in a sequential kinetic mechanism; 5 sequential binding of NADH and crotonoyl CoA by Fab I; increasing inhibition of Fabl by saturated fatty acyl CoA's of increasing chain length; feedback regulatory mechanism of Fab I by saturated fatty acyl CoA's: competitive inhibition by palmitovl CoA versus crotonovl CoA; 10 competitive inhibition by palmitovl CoA versus crotonovl CoA modulation through binding of multiple palmitovl CoA molecules to Fab I; binding of multiple palmitovl CoA molecules to Fab I: negative cooperativity in the binding of CCA; formation of an dimeric quaternary structure: formation of an tetrameric quaternary structure; 15 formation of an oligomeric quaternary structure; binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitoyl coA; and NADH binding to Fab I prior to or simultaneous with ACP binding. 20 11. A method for inhibiting an activity of Fab I polypeptide comprising the steps of contacting a composition comprising said polypeptide with an effective amount of an antagonist that inhibits an activity of Fab I, wherein said activity is selected from the group consisting of: uncompetitive inhibition by Apo-ACP versus NADH (Ki(app); 25 competitive inhibition by Apo-ACP versus crotonoyl CoA; induction of negative cooperativity with respect to CCA binding: use of NADH and NADPH as substrates by Fab I; binding of NADH and NADPH by FabI; oxidation of NADH and NADPH by Fabl: 30 ratio of Kmapp for NADH as compared to NADPH;

use of NADH and crotonoyl CoA as substrates by Fab I in a sequential

kinetic mechanism:

sequential binding of NADH and crotonovl CoA by Fab I: increasing inhibition of Fabl by saturated fatty acyl CoA's of increasing chain length; feedback regulatory mechanism of Fab I by saturated fatty acvl CoA's: 5 competitive inhibition by palmitoyl CoA versus crotonoyl CoA; competitive inhibition by palmitoyl CoA versus crotonovl CoA modulation through binding of multiple palmitoyl CoA molecules to Fab I: binding of multiple palmitoyl CoA molecules to Fab I; negative cooperativity in the binding of CCA: 10 formation of an dimeric quaternary structure; formation of an tetrameric quaternary structure; formation of an oligomeric quaternary structure; binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitovl coA; and 15 NADH binding to Fab I prior to or simultaneous with ACP binding. 12. A method for inhibiting an activity of Fab I, wherein said activity is selected from the group consisting of: uncompetitive inhibition by Apo-ACP versus NADH (Ki(app); competitive inhibition by Apo-ACP versus crotonoyl CoA; 20 induction of negative cooperativity with respect to CCA binding: use of NADH and NADPH as substrates by Fab I; binding of NADH and NADPH by Fabl; oxidation of NADH and NADPH by FabI; ratio of Kmapp for NADH as compared to NADPH; 25 use of NADH and crotonoyl CoA as substrates by Fab I in a sequential kinetic mechanism; sequential binding of NADH and crotonoyl CoA by Fab I: increasing inhibition of FabI by saturated fatty acyl CoA's of increasing chain length; feedback regulatory mechanism of Fab I by saturated fatty 30 acyl CoA's; competitive inhibition by palmitovl CoA versus crotonovl CoA;

competitive inhibition by palmitoyl CoA versus crotonoyl CoA modulation through binding of multiple palmitovl CoA molecules to Fab I: binding of multiple palmitov! CoA molecules to Fab I; negative cooperativity in the binding of CCA; 5 formation of an dimeric quaternary structure; formation of an tetrameric quaternary structure; formation of an oligomeric quaternary structure: binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitovl coA; and 10 NADH binding to Fab I prior to or simultaneous with ACP binding. 13. The method of claim 12 wherein said bacteria is selected from the group consisting of: a member of the genus Staphylococcus. Staphylococcus aureus, a member of the genus Streptococcus, and Streptococcus pneumoniae. 14. A method for inhibiting a growth of bacteria comprising the steps of 15 contacting a composition comprising bacteria with an antibacterially effective amount of an antagonist that inhibits an activity of Fab I, wherein said activity is selected from the group consisting of: uncompetitive inhibition by Apo-ACP versus NADH (Ki(app); competitive inhibition by Apo-ACP versus crotonoyl CoA; 20 induction of negative cooperativity with respect to CCA binding: use of NADH and NADPH as substrates by Fab I: binding of NADH and NADPH by Fabl; oxidation of NADH and NADPH by FabI: ratio of Kmapp for NADH as compared to NADPH; 25 use of NADH and crotonoyl CoA as substrates by Fab I in a sequential kinetic mechanism; sequential binding of NADH and crotonovl CoA by Fab I; increasing inhibition of Fabl by saturated fatty acyl CoA's of increasing chain length; feedback regulatory mechanism of Fab I by saturated fatty 30 acvl CoA's;

competitive inhibition by palmitoyl CoA versus crotonovl CoA;

competitive inhibition by palmitovl CoA versus crotonovl CoA modulation through binding of multiple palmitovl CoA molecules to Fab I; binding of multiple palmitovl CoA molecules to Fab I; negative cooperativity in the binding of CCA; 5 formation of an dimeric quaternary structure; formation of an tetrameric quaternary structure; formation of an oligomeric quaternary structure; binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitovl coA; and 10 NADH binding to Fab I prior to or simultaneous with ACP binding. 15. The method of claim 14 wherein said bacteria is selected from the group consisting of: a member of the genus Staphylococcus, Staphylococcus aureus, a member of the genus Streptococcus, and Streptococcus pneumoniae. 16. A method for inhibiting a Fab I polypeptide comprising the steps of contacting a composition comprising bacteria with an antibacterially effective amount of an 15 antagonist that inhibits an activity of Fab I, wherein said activity is selected from the group consisting of: uncompetitive inhibition by Apo-ACP versus NADH (Ki(app); competitive inhibition by Apo-ACP versus crotonoyl CoA: 20 induction of negative cooperativity with respect to CCA binding; use of NADH and NADPH as substrates by Fab I; binding of NADH and NADPH by FabI; oxidation of NADH and NADPH by Fabl; ratio of Kmapp for NADH as compared to NADPH; 25 use of NADH and crotonoyl CoA as substrates by Fab I in a sequential kinetic mechanism; sequential binding of NADH and crotonovl CoA by Fab I; increasing inhibition of FabI by saturated fatty acyl CoA's of increasing chain length; feedback regulatory mechanism of Fab I by saturated fatty 30 acyl CoA's; competitive inhibition by palmitoyl CoA versus crotonoyl CoA;

> competitive inhibition by palmitoyl CoA versus crotonoyl CoA modulation through binding of multiple palmitoyl CoA molecules to Fab I: binding of multiple palmitoyl CoA molecules to Fab 1: negative cooperativity in the binding of CCA:

5 formation of an dimeric quaternary structure; formation of an tetrameric quaternary structure; formation of an oligomeric quaternary structure; binding of Fab I by pseudo-product inhibitors beta-NADP+ or palmitoyl coA; and

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NADH binding to Fab I prior to or simultaneous with ACP binding. The method of claim 16 wherein said bacteria is selected from the group 17. a member of the genus Staphylococcus, Staphylococcus aureus, a member of consisting of: the genus Streptococcus, and Streptococcus pneumoniae.